Patent French FAMILY ACC. NUM. COUNT: PATENT INFORMATION: DOCUMENT TYPE:

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APPLICATION NO.		FR 1990-14519		WO 1991-FR917		DE, DK, ES, FR, GB, GR, IT, LU, NL, SE	19931013 EP 1992-900187			AT 1992-900187	FR 1990-14519
DATE		19920522	19950303	19920611		, ES, FR, GE	19931013	19981104	R: AT, BE, CH, DE, GB, LI, LU, NL	19981115	
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PATENT NO.		FR 2669338	FR 2669338	WO 9209632	W: CA,	RW: AT, BE, CH,	EP 564477	EP 564477	R: AT,	AT 172983	PRIORITY APPLN. INFO.:

glucose oxidase) for therapeutics and diagnostics. Five specific peptide sequences are claimed. Also claimed is a model for evaluating the efficacy of immunoconjugates. The peptides were used in an ELISA format to test serum samples from FIV-infected and noninfected cats. Results of use of the peptides conjugated to albumin or hemocyanin as immunogens is also reported, as are the preparation and testing of an anti-peptide antibody immunoconjugate with Peptide fragments are disclosed which are derived from the external protein of FIV. Also disclosed are antibodies to the peptide fragments and use of the fragments and the antibodies (alone or conjugated to other substances, e.g. W 19911120 WO 1991-FR917 glucose oxidase. AB

L13 ANSWER 11 OF 11 ZCAPLUS COPYRIGHT 2007 ACS on STN ACCESSION NUMBER: 1992:424420 ZCAPLUS FULL-text 117:24420 DOCUMENT NUMBER:

feline immunodeficiency virus
Avrameas, Alexandre, Güillet, Jean Gerard;
Chouchane, A. Donny; Moraillon, Anne; Sonigo, Pierre;
Strosberg, A. Donny Localization of three epitopes of the env protein of

AUTHOR (S):

SOURCE:

Inst. Cochin Genet. Mol., Univ. Paris VII, Paris, Fr. Molecular Immunology (1992), 29(5), 565-72 CODEN: MOIMD5; ISSN: 0161-5890 CORPORATE SOURCE:

English DOCUMENT TYPE:

Tentative. homologies with the immunodominant epitope sites in simian virus (SIV) or human immunodeficiency virus (HIV) such as the V3 loop, the site of cleavage between surface envelope protein (SU) and transmembrane envelope protein (TM), and sites of N-glycosylation were thus identified. Five peptides corresponding to potential epitopes were synthesized. Four out of 5 peptides (P99, P100, P101, P103) were from the FIV surface envelope protein (SU). The last one (P102) was from the FIV transmembrane envelope protein Three of these peptides (P99, P100, and P102) were recognized in ELISA by almost all the sera from infected cats. The peptide from TM (102) was .using several epitope prediction programs based on profiles of hydrophilicity, antigenicity, and probability of residues lying on the protein surface. peptide P99 and P100 (from SU) were recognized mainly by sera from naturally infected cats. Thus, peptides P99 and P100 from SU and P102 from TM recognized by sera from both naturally infected and inoculated cats, whereas The envelope protein of the feline immunodeficiency virus (FIV) was analyzed constitute epitopes on the FIV env protein. LANGUAGE: ΑB

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This file contains CAS Registry Numbers for easy and accurate 'OBI' IS DEFAULT SEARCH FIELD FOR 'ZCAPLUS' FILE substance identification.

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JUS COPYRIGHT 2007 ACS on STN 2006:1099900 ZCAPLUS FULL-text 146:21082 The 150-kilobase genome of the bacterial endosymbiont LII ANSWER 1 OF 8 ZCAPLUS
ACCESSION NUMBER: 200
DOCUMENT NUMBER: 146
TITLE: The

genome has a high coding d. (97%) with many overlapping genes and reduced gene length. Genes for translation, and maino acid biosythreesis are relatively well represented, but numerous genes considered essential for life are missing, suggesting that Carsonella may have achieved organelle-like status. It is Previous studies have suggested that the minimal cellular genome could be as circular chromosome of 159,662 base pairs, averaging 16.5% GC content. It the smallest and most AT-rich bacterial genome characterized to date. The Environmental Molecular Biology, RIKEN, Wako, Saitama, Hideohiro; Ishikawa, Hajime; Dunbar, Helen E.; Moran, small as 400 kilobases. The present study reports the complete genome sequence of the psyllid symbiont Carsonella ruddii, which consists of a American Association for the Advancement of Science 915063-08-0 915063-23-9 915064-55-0 915063-03-5 915063-38-6 915063-58-0 915063-73-9 915063-93-3 915063-98-8 915064-03-8 915064-08-3 915064-15-2 915064-20-9 915062-98-5 915063-28-4 915063-68-2 915063-78-4 915063-83-1 915063-88-6 915063-13-7 915063-33-1 915063-43-3 15063-48-6 915063-53-5 915063-63-7 915064-25-4 351-0198, Japan Science (Washington, DC, United States) (2006). 915064-30-915064-35-915064-45-915064-10-7 Nakabachi, Atsushi; Yamashita, Atsushi; Toh, 915064-02-7 915064-19-6 915063-62-6 915063-72-8 915063-82-0 915063-87-5 915063-92-2 915063-97-7 915064-07-2 915064-14-1 915064-24-3 915064-29-8 915064-39-0 915063-02-4 915063-07-9 915063-12-6 915063-47-7 915063-52-4 915063-57-9 915063-77-3 915062-92-9 915062-97-4 915063-17-1 915063-22-8 915063-27-3 915063-32-0 915063-37-5 915063-42-2 915063-67-1 915064-49-2 0036-8075 GTPase (Carsonella ruddii strain PV) Nancy A.; Hattori, Masah 314(5797), 267 CODEN: SCIEAS; ISSN: 915064-01-6 915064-18-5 915064-48-1 915062-81-6 915062-86-1 915063-01-3 915063-06-8 915063-11-5 915063-16-0 915063-21-7 915063-26-2 915063-31-9 915063-36-4 915063-41-1 915063-46-6 915063-51-3 915063-56-8 915063-61-5 915063-66-0 915063-71-7 915063-76-2 915063-81-9 915063-86-4 915063-91-1 115064-06-1 915064-28-7 915064-38-9 915062-91-8 915062-96-3 915064-57-2 915064-58-3 Section cross-reference(s): 10 English Journal 3-3 (Biochemical Genetics) 915062-80-5 915062-85-0 915062-95-2 915063-20-6 915063-40-0 915063-45-5 915063-65-9 915063-70-6 915063-80-8 915063-90-0 915064-00-5 915064-05-0 915064-27-6 915064-37-8 915063-00-2 915063-05-7 915063-15-9 915063-30-8 915063-50-2 .915063-55-7 915063-85-3 915063-95-5 915064-17-4 915064-32-3 915063-10-4 915063-25-1 915063-60-4 915063-75-1 915064-22-1 915062-90-7 915063-35-3 CORPORATE SOURCE: 915062-84-9 915063-04-6 915063-24-0 915063-29-5 915062-89-4 915063-09-1 915063-14-8 915063-49-9 915063-54-6 915063-74-0 915063-79-5 915063-99-9 915064-11-8 915064-21-0 915064-26-5 915064-46-9 915063-44-4 915063-59-1 915063-69-3 915063-89-7 915064-09-4 915064-16-3 915064-31-2 915063-39-7 915063-84-2 915064-51-DOCUMENT TYPE: PUBLISHER: AUTHOR (S) LANGUAGE: SOURCE: ပ္ပ AB

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915064-59-4

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915064-60-7 RL: BSU (Biological study, unclassified); PRP (Properties); BIOL (Biological study) (anino acid sequence; complete sequence of 160-kilobase genome of bacterial endosymbiont Carsonella ruddis) STHERE ARE 5 CITED REFERENCES AVAILABLE FOR THIS RECORD: RECORD: ALL CITATIONS AVAILABLE IN THE RE FORMAT	8 2CAPLUS COPYRIGHT 2007 ACS on STN: 2006:769164 2CAPLUS Full-text 145:224845 Anti-angiogenic peptides and methods of use thereof Rastelli, Luca, Landin, Judith; Malyankar, Uriel; Kitson, Richard, Corso, Malissa; Brunson, Kenneth); USA. USA. U.S. Pat. Appl. Publ., 48pp., Contin-par PCT/USOS/18959. CODEN: USXXCO Patent English COUNT: 2	KIND DATE APPLICATION NO. DATE	:	14 A2 20060427 WO 2005-US36959 20051014 14 A3 20060810	AG, AL, AM, AT, AU, AZ, BA, BB, BG, BR, BM, BY, BZ, CA, CH, CO, CR, CU, CZ, DE, DK, DM, DZ, EC, EE, EG, ES, FI, GB, GD,	GH, GM, HR, HU, ID, IL, IN, IS, JP, KE, KG, KM, KP,	NG, NI, NO, NZ, OM, PG, PH, PL, PT, RO, RU, SC, SD, SE,	SL, SM, SY, TJ, TM, TN, TR, ZA, ZM, ZW		CG, CI, CM, GA, GN, GQ, GW, ML, MR, NE, SN, TD, TG, BW,	KE, LS, MW, MZ, NA, SD, SL, SZ, TZ, UG, ZM, ZW, AM, AZ, BY, KZ, MD, RU, TJ, TM	INFO.:	MAJ genic peptic cells are	receptor (al to its recep	inhibit, VBGF, bFGF, or integrin activation of endothelial cells in angiogenesis-associated diseases such as cancer, leukemia, multiple myeloma, inflammatory diseases, eye diseases and skin disorders.	\$30350000 (cology)	: 63 144095-01-2 147236-19-9	190894-91-8 205117-83-5 211106-37-5	243961-51-5 247111-51-9 268214-27-3 268539-66-8 353483-40-6 359636-54-7 364618-18-8 364618-24-6	364618-26-8 492444-99-2 494228-18-1	573664-51-4 875516-71-5 875517-64-9 875757-92-9 884508-79-6 884508-80-9 884508-81-0 884508-82-1
915064-60-7 RL: BSU (Biological study, (Biological study) (anino acid sequence, c bacterial endosymbiont REFERENCE COUNT:	L11 ANSWER 2 OF 8 ZCAPLUS CO ACCESSION NUMBER: 2006:7 DOCUMENT NUMBER: 145:22 TITLE: Anti-a INVENTOR(S): Rastel INVENTOR(S):		PATENT NO. KIND	US 2006172941 Al	WO 2006044614 A2 WO 2006044614 A3	CR, AM,	GH, GM, HR,	NG, NI, NO,	SM, SY, ZM, ZW	BG, CH, LT, LU,	CG, CI, CM,	LS, MW, MD, RU,	INFO.:	OTHER SOURCE(S): AB Anti-angiogenic peptides that infende endothelial cells are disclosed.	binding to the VEGFR2 rece KDR) and bFGF binding to	inhibit, VEGF, bFGF, or in angiogenesis-associated di inflammatory diseases, eve	INCL 514012000; 530350000 CC 1-6 (Pharmacology)	Section cross-reference(s) III1793-75-0 143740-07-2		220334-13-4 243961-51-5 272121-15-0 353483-40-6		502719-76-8 573664-51-4 884508-78-5 884508-79-6

884508-85-4 884508-86-5 884508-87-	884508-90-1	902768-66-5 902768-67-6	902768-71-2 902768-72-3	902768-76-7 902768-77-8 9	903912-64-1	904743-64-2 904743-65-3	tted 904743-67-5 904743-68-6 904743-69-7	l activity); PRP (Properties); THU (Therapeutic		(anti-angiogenic peptides and methods of use thereof)	US COPYRIGHT 2007 ACS on STN 2006:647420 ZCAPLUS PUll-text 145:77446	Complete genome sequence of the chlorarachniophyte nucleomorph: Nature's smallest nucleus	<pre>Gilson, Paul R.; Su, Vanessa, Slamovits, Claudio H.; Reith, Michael E.; Keeling, Patrick J.; McFadden,</pre>	Geoiffey 1. Infection and Immunity Division, The Walter and Eliza Hall Institute of Medical Research, Parkville, 3050,	AUSTRALIA Proceedings of the National Academy of Sciences of the United States of America (2006) 103 (26) 9566-9571)EN: PNASA6; ISSN: 0027-8424	National Academy of Sciences	irnal	of plastids into different heterotrophic protists created	ine and	s, and radically altered the biosphere: The origins of	are	two examples provine unique snapshors ction, because they retain a vestige of	endosymbiont nucleus known as the nucleomorph. These are chlorarachniophytes	and cryptomonads, which acquired their plastids from a green and red alga resp. To allow comparisons between them, the mucleomorph genome from the	chlorarachniophyte Bigelowiella natans was sequenced: at a mere 373,000 bp and	with only 331 genes, the smallest nuclear genome known and a model for extreme	d genes with numerous overlaps. The genome is repl		20, or 21 nt in length. These pygmy introns are shown to be miniaturized versions of normal-sized introns present in the endosymbiont at the time of		leomorph genes are housekeeping entities, presumably	Chlorarachniophyte plastids are thus serviced by 3 different genomes (plastid,	nucleomorph, and host nucleus) requiring remarkable coordination and targeting. Although originating by 2 independent endosymbloses.	chlorarachniophyte and cryptomonad nucleomorph genomes have converged upon	similar architectures but differ in many mol. details that reflect trajectories to hypercompaction and reduction The B. natans	uence is deposited in GenBank/EMBL/I		:(s): 6, 10
884508-84-3	884508-89-8	902768-65-4	902768-70-1	902768-75-6	902768-80-3	904743-63-1	biotinylated	nacological	iological st	ogenic peptio	ZCAPL	Comple	Gilson		Austro Proce	CODEN	Natio	Journal Frelish	ion of plastic	lgae that di	nvironments,	Tacids	dnes. nowev	nucleus know	ads, which a	phyte Bigelo	131 genes, the	nsely packed			nteen nucleo	other nucleo	phyte plasti	and host nuc	phyte and cr	milar archit ajectories t	Jenome sequer	(Biochemical Genetics)	-reference(s
884508-83-2	884508-88-7	902768-64-3	902768-69-8	902768-74-5	902768-79-0	904743-62-0	904743-56-4D, 904743-71-1	RL: PAC (Phare	use); BIOL (B:	(anti-angi	L11 ANSWER 3 OF 8 ACCESSION NUMBER: DOCUMENT NUMBER:	TITLE:	AUTHOR(S):	CORPORATE SOURCE: '	SOURCE:		PUBLISHER:	DOCUMENT TYPE:	AB The introduction	lineages of a	freshwater en	chese secondary pro	secondary-end	endosymbiont	and cryptomon	chlorarachnic	with only 331	containing de	with 852 introns, but th	20, or 21 nt versions of n	capture. Seve	plastid. The	Chlorarachnic	nucleomorph,	chlorarachnic	remarkably si 2 distinct tr	nucleomorph	CC 3-3 (Biochemical Geneti	Section cross-reference(s):

6.62-6 892335-83-0 892335-88-5 6.74-4 892335-88-5 892535-88-5 6.97-6 89235-88-5 892535-88-5 6.97-6 89235-88-5 89253 6.97-6 89235-98-7 89253 6.12-8 89235-113-7 89253 6.17-3 892336-118-4 89253 6.17-3 892336-118-4 89253 6.17-3 892336-13-1 89253 6.17-4 892336-13-3 89253 6.47-6 892336-13-3 89253 6.47-7 892336-13-3 89253 6.47-8 892336-13-4 89253 6.47-9 892336-13-3 89253 6.47-9 892336-13-4 89253 6.47-9 892336-83-3 89253 6.47-9 892336-83-3 89253 6.48-8 892336-83-3 89253 6.98-9 892337-94-4 89253 6.98-9 892237-24-5 89253 7.18-7 892237-24-7 89253 7.28-7	892535-8 892535-9	3 892535	-8 892536-00 -8 892536-05	-3 892536-10-	892536-1	892536-20-	892536-2	-892536-30-	892536-35-	892536-40-	892536-4	892536-50-	892536-55-	892536-60	892536-65-	892536-70-	892536-75-	-7 892536-80-	-4 892536-85-	-2 892536-91	-7 892536-96-	-7 892537-01-	-2 892537-06-	-9 892537-11-	-4 892537-16	-1 892537-21-	-6 892537-26-	-3 892537-31-	-8 892537-36-	-14-1600 -14-1600	-7 892537-51	-2 892537-56-	-9 892537-61-	8925	892537-71-		892537-8	892537-85-	892537-91-	892537-96-	538-0	-5 892538-06-	892538-11-	892538-16-		(Properties) - BIOI.	
5. 82.9 5. 82.9 6. 6. 12.8 6. 12.8 6. 12.1 8. 82.5 6. 12.1 8. 82.5 8. 82.5 6. 83.1 8. 82.5 8. 83.5 8. 83.5	35-83-0 892535-8 35-88-5 892535-8	35-93-2 892535-9	35-98-7 892535-9 36-03-7 892536-0	36-08-2 892536-0	6-13-9 892536-1	5-18-4 892536-1	5-23-1 892536-2	5-28-6 892536-2	6-33-3 892536-3	36-38-8 892536-3	36-43-5 892536-4	36-48-0 892536-4	36-53-7 892536-5	36-58-2 8,92536-5	36-63-9 892536-6	36-68-4 892536-6	36-73-1 892536-7	36-78-6 892536-7	36-83-3 892536-8	36-89-9 892536-9	36-94-6 892536-9	36-99-1 892537-0	37-04-1 892537-0	37-09-6 892537-1	37-14-3 892537-1	37-19-8 892537-2	37-24-5 892537-2	37-29-0 892537-3	37-34-7 892537-3	3/-39-2 89253/-4	37-44-9 892537-4 77-44-4 892537-5	37-54-1 892537-5	17-59-6 892537-6	37-64-3 892537-6	37-69-8 892537-7	-74-5 892537-75-	37-78-9 892537-7	37-83-6 892537-8	37-88-1 892537-8	37-94-9 892537-9	37-99-4 892538-0	38-04-4 892538-0	38-09-9 892538-1	38-14-6 892538-	38-19	ceified). DDD	
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Altherr, Michael R.; Bhotika, Smriti S.; Bruce, David, Campbell, Connie S.; Campbell, Mary L.; Chen, Jin; Chertkov, Olga; Cleland, Cathy; Dimitrijevic, Mira; Doggett, Norman A.; Pawcett, John J.; Glavina, Tijana;

Bacillus thuringiensis isolates closely related to

Han, Cliff S.; Xie, Gary; Challacombe, Jean F.;

Bacillus

AUTHOR (S):

H

Goodwin, Lynne A.; Hill, Karen K.; Hitchcock, Penny;

Paul J.; Keim, Paul; Kewalramani, Avinash Longmire, Jon; Lucas, Susan; Malfatti,

Jackson, Ramesh;]

Stephanie; McMurry, Kim; Meincke, Linda J.; Misra, Monica; Moseman, Bernice L.; Mundt, Mark; Munk, A.

Christine; Okinaka, Richard T.; Parson-Quintana, B.; Reilly, Lee Philip; Richardson, Paul; Robinson, Donna L.; Rubin, Eddy; Saunders, Elizabeth; Tapla, Roxanne;

Tice, Hope; Ticknor, Lawrence O.; Wills, Patti L.; Brettin, Thomas S.; Gilna, Paul

Tesmer, Judith G.; Thayer, Nina; Thompson,

Laboratory, Los Alamos, NM, 87545, USA Journal of Bacteriology (2006), 188(9), 3382-3390

CODEN: JOBAAY; ISSN: 0021-9193 American Society for Microbiology

Journal

DOCUMENT TYPE:

PUBLISHER:

SOURCE:

DOE Joint Genome Institute Los Alamos National

CORPORATE SOURCE:

(amino acid sequence; complete genome sequence of Bigelowiella natans exhibits the smallest known genome, ultrasmall introns, and genes that function in the chlorarachniophyte plastid)

REFERENCE COUNT:

11 RECORD. ALL CITATIONS AVAILABLE FOR THIS REFORMAT

LII ANSWER 4 OF 8 ZCAPLUS COPYRIGHT 2007 ACS on STN
ACESSION NUMBER: 2006:412218 ZCAPLUS FULL-text
DOCUMENT NUMBER: 144:381027
TITLE: Pathogenomic sequence analysis of Bacillus cereus and

1

sequence homogeneity, environmental isolates of B. cereus and B. thuringiensis exhibit extensive genetic diversity. This report describes the sequencing and comparative anal. of the genomes of two members of the B. cereus group, B. thuringiensis 97-27 subsp. konkukian serotype H34, isolated from a necrotic human wound, and B. cereus B31, which was isolated from a swab of a zebra carcass in Namibia. These two strains, when analyzed by amplified fragment length polymorphism within a collection of over 300 of B. cereus, B. thuringiensis, and B. anthracis isolates, appear closely related to B. anthracis. The B. cereus Bill isolate appears to be the nearest relative to B. anthracis identified thus far. Whole-genome sequencing of B. thuringiensis 97.27 and B. cereus Bill was undertaken to identify shared and unique genes among these isolates in comparison to the genomes of pathogenic strains B. one of two records for this document necessitated by the large number of index nos. AE017355 and CP000047, and the B. cereus E33L and five plasmids sequences are deposited under CP000001 and CP000040-CP000044. [This abstract record is plasmid pBT9727 sequences are deposited in GenBank/EMBL/DDBJ under accession Bacillus anthracis, Bacillus cereus, and Bacillus thuringiensis are closely related gram-pos., spore-forming bacteria of the B. cereus sensu lato group. While independently derived strains of B. anthracis reveal conspicuous anthracis Ames and B. cereus G9241 and nonpathogenic strains B. cereus ATCC The B. thuringiensis 97-27 and its 31466 82-amino acid) 883428-62-4, Protein (plasmid id) 883428-63-5 883428-64-6, Transposase (plasmid 883428-65-7, Transposase (plasmid pB331466 gene tnp) Comparison of these genomes revealed differences in terms of virulence, metabolic competence, structural components, and regulatory mechanisms. The B. thuringiensis 97-27 a 883428-61-3, entries required to fully index the document and publication system 883428-56-6, Thioredoxin 883428-67-9 883428-68-0, Protein (plasmid pE33L466 (plasmid pE3314466) 883428-57-7 883428-58-8 883428-59-9 883428-60-2, Protein (plasmid pE331466 78-amino acid) 8834; 883428-54-4 Protein (plasmid pE33L466 82-amino acid) Protein (plasmid pE33L466 87-amino acid) 883428-53-3 Section cross-reference(s): 6, 10, 14 883428-51-1 883428-52-2 883428-53-10987 and B. cereus ATCC 14579. English (Biochemical Genetics) pE33L466 73-amino acid) pE33L466 gene tnp) 883 constraints. 883428-66-8 LANGUAGE: ပ္ပ H

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883429-53-6 883429-64-7, Protein (plasmid pE331466 67-amino acid)
883429-55-8 883429-56-9 883429-57-0, Phosphoesterase (plasmid pE331466)
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(Biological study)

(Amino acid sequence, pathogenomic sequence anal. of complete genomes of Bacillus cereus and Bacillus thuringiensis isolates closely related to Bacillus anthracis)

THERE ARE 41 CITED REFERENCES AVAILABLE FOR THIS RECORD. ALL CITATIONS AVAILABLE IN THE RE FORMAT

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endothelial cells are disclosed. Such peptides maybe used to inhibit VEGF binding to the VEGFR2 receptor (also known as the kinase domain receptor or KRR) and bEGF binding to its receptor. Such peptides may also be used to inhibit VEGF, bFGF, or integrin activation of endothelial cells in
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Heather; Nelson, Siri; Norbertczak, Halina; Oliver,
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Horn, David; Huang, Yiting; Klages, Sven; Knights,
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machinery for synthesis of complex surface glycoconjugates. The organization of protein-coding genes into long, strand-specific, polycistronic Clusters and lack of general transcription factors in the L. major, Trypanosoma brucei, and Trypanosoma cruzi (Tritryp) genomes suggest that the mechanisms regulating RNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       other eukaryotes, although the trypanosomatids appear capable of chromatin remodeling. Abundant RNA-binding proteins are encoded in the Tritryp genomes, consistent with active posttranscriptional regulation of gene expression. The
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                                                                                                                                                                                                                                                                                                             RNA genes, 39 pseudogenes, and 8272 protein-coding genes were predicted, of which 36% can be ascribed a putative function. These include genes involved in host-pathogen interactions, such as proteolytic enzymes, and extensive
                                                                                                                                                                                                                                                                                          haploid genome of Leishmania major (Friedlin strain) were sequenced and 911
                                                                                                                                                                                                                                  Leishmania species cause a spectrum of human diseases in tropical and subtropical regions of the world. The 36 chromosomes of the 32.8-megabase
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Barrell, Bart; Myler, Peter J.
Wellcome Trust Genome Campus, Wellcome Trust Sanger
Institute, Hinxton, Cambridgeshire, CB10 15A, UK
                                                                                                                                                       American Association for the Advancement of Science
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	libraries generated from various plants, including Zea mays, Glycine max,	erated 1	ron:	various plan	its, .	including	Zea may	s, Glyc	ine max,	
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	biassica mapus, gossyptum missucum, cucumis sacivis, bilium assacio, o bicolor, Chlorella sorokiniana, Cuphea pulcherrima, and Allium porrum.	rella sc	rokir	niana, Cuphe	מים	lcherrima,	and Al	lium po	rrum. The	

This invention provides 36,564 polynucleotide sequences isolated from cDNA libraries generated from various plants, including Zea mays, Glycine max, Arabidopsis thaliana, Lycopersicon esculentum, Oryza sativa, Triticum aesticum, Euglena gracilis, Chlorella vulgaris, Schizochytrium aggregatum, Brassica napus, Gossypium hireutum, Cucumis sativis, Lilium asiatic, Sorghum bicolor, Chlorella sorghumia, Cuphea pulcherrima, and Allium porture. The open reading frame in each polynucleotide sequence is identified by a combination of predictive and homol. based methods. Functions of polypoptides encoded by the polynucleotides sequences are determined using a hierarchical classification tool, termed FuncAT annotation at gargeries are identified by propertises are identified from their FuncAT annotations of polypoptides for their funcAT annotations. [This abstract record is one of 19 records for this document necessitated by the large of index entries required to fully index the document and publication system

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INCL 800289000, 530370000, 536023600, 435200000
CC 3-3 (Biochemical Genetics)

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RL: BSU (Biological study, unclassified); BUU (Biological use, unclassified); PRP (Properties); BIOL (Biological study); USES (Uses) (amino acid sequence; nucleic acids and encoded proteins associated with plants and their uses for plant improvement)

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ACCESSION NUMBER: 2003:796119 ZCAPLUS FULL-text
DOCUMENT NUMBER: 139:312392
TITLE: Biological affinity-based drug delivery systems
INVENTOR(8): Panitch, Alyssa; Seal, Brandon
PATENT ASSIGNEE (5): USA

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FILE HOME

FILE REGISTRY

Property values tagged with IC are from the ZIC/VINITI data file provided by Infochem.

HIGHEST RN 940883-34-1 HIGHEST RN 940883-34-1 2 JUL 2007 2 JUL 2007 STRUCTURE FILE UPDATES: DICTIONARY FILE UPDATES: New CAS Information Use Policies, enter HELP USAGETERMS for details.

ISCA INFORMATION NOW CURRENT THROUGH December 2, 2006

Please note that search.term pricing does apply when conducting SmartSELECT searches.

predicted properties as well as tags indicating availability of experimental property data in the original document. For information on property searching in REGISTRY, refer to: REGISTRY includes numerically searchable data for experimental and

http://www.cas.org/support/stngen/stndoc/properties.html

FILE ZCAPLUS

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FILE COVERS 1907 - 3 Jul 2007 VOL 147 ISS 2 FILE LAST UPDATED: 2 Jul 2007 (20070702/ED)

New CAS Information Use Policies, enter HELP USAGETERMS for details..

This file contains CAS Registry Numbers for easy and accurate substance identification.

LAST RELOADED: Jun 29, 2007 (20070629/UP). FILE STNGUIDE FILE CONTAINS CURRENT INFORMATION.

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NEW CAS INFORMATION USE POLICIES, ENTER HELP USAGETERMS FOR DETAILS.

27

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COST IN U.S. DOLLARS

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FULL ESTIMATED COST

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STRUCTURE FILE UPDATES: 1 JUL 2007 HIGHEST RN 940612-32-8 DICTIONARY FILE UPDATES: 1 JUL 2007 HIGHEST RN 940612-32-8

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The following are valid formats:

Substance information can be displayed by requesting individual fields or predefined formats. The predefined substance formats are: (RN = CAS Registry Number)

REG - RN

L2

SAM - Index Name, MF, and structure - no RN FIDE - All substance data, except sequence data

IDE - FIDE, but only 50 names SQIDE - IDE, plus sequence data

SQIDE3 - Same as SQIDE, but 3-letter amino acid codes are used - Protein sequence data, includes RN SOD - Same as SQD, but 3-letter amino acid codes are used SOD3 SON - Protein sequence name information, includes RN CALC - Table of calculated properties - Table of experimental properties EPROP PROP - EPROP and CALC Any CA File format may be combined with any substance format to obtain CA references citing the substance. The substance formats must be cited first. The CA File predefined formats are: ABS -- Abstract APPS -- Application and Priority Information BIB -- CA Accession Number, plus Bibliographic Data CAN -- CA Accession Number CBIB -- CA Accession Number, plus Bibliographic Data (compressed) IND -- Index Data IPC -- International Patent Classification PATS -- PI, SO -- BIB, IPC, and NCL STD IABS -- ABS, indented, with text labels IBIB -- BIB, indented, with text labels ISTD -- STD format, indented OBIB ----- AN, plus Bibliographic Data (original) OIBIB ----- OBIB, indented with text labels SBIB ----- BIB, no citations SIBIB ----- IBIB, no citations The ALL format gives FIDE BIB ABS IND RE, plus sequence data when it is available. The MAX format is the same as ALL. The IALL format is the same as ALL with BIB ABS and IND indented, with text labels. For additional information, please consult the following help messages: HELP DFIELDS -- To see a complete list of individual display fields. HELP FORMATS -- To see detailed descriptions of the predefined formats. ENTER DISPLAY FORMAT (IDE): end => s 12 and sql=18 176306 SQL=18 0 L2 AND SQL=18 L3 => d 12 sqide 1-6 ANSWER 1 OF 6 REGISTRY COPYRIGHT 2007 ACS on STN L2 RN 921682-97-5 REGISTRY Protein (Oryza sativa japonica strain Nipponbare gene Os07g0164800) INDEX NAME) OTHER NAMES: GenBank BAF20877 CNGenBank BAF20877 (Translated from: GenBank AP008213) CN FS PROTEIN SEQUENCE SQL 275

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Absolute stereochemistry.

CI SR

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FS SQL

SEQ

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PAGE 2-A

PAGE 3-A

PAGE 5-A

PAGE 6-A

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- 1 REFERENCES TO NON-SPECIFIC DERIVATIVES IN FILE CA
- 2 REFERENCES IN FILE CAPLUS (1907 TO DATE)

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DT.CA CAplus document type: Patent

RLD.P Roles for non-specific derivatives from patents: BIOL (Biological study); PREP (Preparation); PRP (Properties)

Absolute stereochemistry.

PAGE 3-A

PAGE 5-A

PAGE 6-A

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- L2 ANSWER 6 OF 6 REGISTRY COPYRIGHT 2007 ACS on STN

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RELATED SEQUENCES AVAILABLE WITH SEQLINK

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COST IN U.S. DOLLARS

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TOTAL

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COST IN U.S. DOLLARS

ENTRY SESSION

FULL ESTIMATED COST

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FILE COVERS 1907 - 2 Jul 2007 VOL 147 ISS 2 FILE LAST UPDATED: 1 Jul 2007 (20070701/ED)

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This file contains CAS Registry Numbers for easy and accurate substance identification.

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L4 7 L2

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     La Rosa, Thomas J.; Kovalic, David K.; Zhou, Yihua; Cao, Yongwei; Wu, Wei;
IN
     Boukharov, Andrey A.; Barbazuk, Brad W.
PA
     U.S. Pat. Appl. Publ., 14 pp., Cont.-in-part of U.S. Ser. No. 837,604.
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TI Soybean nucleic acids and encoded proteins associated with transcription in plants and their uses for plant improvement

IN La Rosa, Thomas J.; Zhou, Yihua; Kovalic, David K.; Cao, Yongwei

PA USA

SO U.S. Pat. Appl. Publ., 15 pp., Cont.-in-part of U.S. Ser. No. 985,678, abandoned.

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